

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
(A) ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY
(B) STREET: 1007 MARKET STREET
(C) CITY: WILMINGTON
(D) STATE: DELAWARE
(E) COUNTRY: UNITED STATES OF AMERICA
(F) ZIP: 19898
(G) TELEPHONE: 302-992-4926
(H) TELEFAX: 302-773-0164
(I) TELEX: 6717325
- (ii) TITLE OF INVENTION: PLANT SUGI HOMOLOGS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: DISKETTE, 3.50 INCH
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
(D) SOFTWARE: MICROSOFT WORD VERSION 7.0A
- (v) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/893,401
(B) FILING DATE: JULY 11, 1997
- (vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: MAJARIAN, WILLIAM R.
(B) REGISTRATION NUMBER: 41,173
(C) REFERENCE/DOCKET NUMBER: BB-1095-A

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Soybean

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT CTT GTA GGA GTT GAA CTG AAG CAT GCG GCG GAG GGC GTA CCG	48
Met Ala Leu Val Gly Val Glu Leu Lys His Ala Ala Glu Gly Val Pro	
1 5 10 15	
GAG GCG AAT TGC TCC GCC AAG CCC ACC AAG CAG GGC GAG GGC CTC CGC	96
Glu Ala Asn Cys Ser Ala Lys Pro Thr Lys Gln Gly Glu Gly Leu Arg	
20 25 30	
CAC TAC TAT TCT CTC AAC ATC CAC GAG CAT CAG CTC CTT CTT CGC CAA	144
His Tyr Tyr Ser Leu Asn Ile His Glu His Gln Leu Leu Leu Arg Gln	
35 40 45	
AAG ACT CAT AAC CTC AAC CGT CTC GAG GCT CAG AGA AAC GAC CTC AAT	192
Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg Asn Asp Leu Asn	
50 55 60	
TCT AGG GTG AGG ATG CTG CGC GAA TTA CAG CTT CTG CAG GAA CCC	240
Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro	
65 70 75 80	
GGC TCT TAT GTC GGT GAA GTT GTC AAA GTA ATG GGC AAG AAC AAA GTC	288
Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly Lys Asn Lys Val	
85 90 95	
CTT GTC AAG GTC CAC CCA GAA GGA AAA TAT GTT GTT GAC ATT GAC AAA	336
Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys	
100 105 110	
AAT ATT GAC ATT ACA AAG ATT ACT CCA TCC ACT AGA GTT GCA CTC CGC	384
Asn Ile Asp Ile Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg	
115 120 125	
AAC GAC AGT TAT GTT CTT CAC TTA GTT CTG CCA AGT AAA GTT GAT CCA	432
Asn Asp Ser Tyr Val Leu His Leu Val Leu Pro Ser Lys Val Asp Pro	
130 135 140	
TTG GTC AAT CTG ATG AAA GTT GAG AAA GTT CCC GAT TCT ACA TAT GAC	480
Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp	
145 150 155 160	
ATG ATT GGT GGT TTA GAC CAG CAA ATT AAA GAA ATA AAA GAG GTC ATT	528
Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile	
165 170 175	
GAG CTA CCA ATC AAA CAT CCT GAG CTG TTT GAA AGT CTT GGA ATT GCA	576
Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala	
180 185 190	

CAA CCA AAG GGT GTC CTG CTC TAT GGG CCA CCT GGT ACA GGT AAA ACA Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr 195 200 205	624
TTG TTG GCT AGG GCA GTG GCT CAT CAT ACT GAC TGT ACA TTC ATC AGG Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg 210 215 220	672
GTG TCT GGT TCT GAG TTA GTT CAG AAA TAC ATT GGA GAA GGT TCT AGA Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg 225 230 235 240	720
ATG GTC AGG GAA CTT TTT GTT ATG GCC AGG GAA CAT GCT CCA TCA ATT Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile 245 250 255	768
ATC TTC ATG GAT GAA ATT GAC AGT ATT GGA TCT GCT CGG ATG GAA TCT Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser 260 265 270	816
GGA AGT GGC AAC GGT GAT AGT GAG GTA CAG CGT ACT ATG CTG GAA CTT Gly Ser Gly Asn Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu 275 280 285	864
CTC AAC CAG TTG GAT GGA TTT GAA GCT TCA AAT AAG ATC AAG GTT TTG Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val Leu 290 295 300	912
ATG GCC ACC AAT CGG ATT GAT ATC CTG GAT CAA GCC CTC CTT AGA CCA Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro 305 310 315 320	960
GGA CGG ATA GAC CGG AAA ATT GAA TTT CCA ACC CCT AAT GAA GAG TCT Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Thr Pro Asn Glu Glu Ser 325 330 335	1008
CGG CTG GAT ATT TTG AAA ATC CAT TCT AGA AGA ATG AAT TTA ATG CGT Arg Leu Asp Ile Leu Lys Ile His Ser Arg Arg Met Asn Leu Met Arg 340 345 350	1056
GGC ATT GAT TTG AAG AAG ATT GCC GAG AAG ATG AAT GGA GCA TCT GGT Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser Gly 355 360 365	1104
GCT GAA CTT AAG GCT GTT TGC ACT GAA GCT GGA ATG TTT GCT TTG AGG Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg 370 375 380	1152
GAG CGG AGG GTA CAC GTG ACT CAG GAG GAT TTT GAG ATG GCC GTG GCG Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala 385 390 395 400	1200
AAG GTG ATG AAA AAG GAG ACT GAA AAA AAC ATG TCA TTG CGG AAG TTG Lys Val Met Lys Lys Glu Thr Glu Lys Asn Met Ser Leu Arg Lys Leu 405 410 415	1248
TGG AAG Trp Lys	1254

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Val Gly Val Glu Leu Lys His Ala Ala Glu Gly Val Pro
 1 5 10 15

Glu Ala Asn Cys Ser Ala Lys Pro Thr Lys Gln Gly Glu Gly Leu Arg
 20 25 30

His Tyr Tyr Ser Leu Asn Ile His Glu His Gln Leu Leu Leu Arg Gln
 35 40 45

Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg Asn Asp Leu Asn
 50 55 60

Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro
 65 70 75 80

Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly Lys Asn Lys Val
 85 90 95

Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys
 100 105 110

Asn Ile Asp Ile Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg
 115 120 125

Asn Asp Ser Tyr Val Leu His Leu Val Leu Pro Ser Lys Val Asp Pro
 130 135 140

Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp
 145 150 155 160

Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile
 165 170 175

Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala
 180 185 190

Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr
 195 200 205

Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg
 210 215 220

Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg
 225 230 235 240

Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile
 245 250 255

Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser
 260 265 270

Gly Ser Gly Asn Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu
 275 280 285

Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val Leu
 290 295 300

Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro
 305 310 315 320

Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Thr Pro Asn Glu Glu Ser
325 330 335

Arg Leu Asp Ile Leu Lys Ile His Ser Arg Arg Met Asn Leu Met Arg
340 345 350

Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser Gly
355 360 365

Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg
370 375 380

Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala
385 390 395 400

Lys Val Met Lys Lys Glu Thr Glu Lys Asn Met Ser Leu Arg Lys Leu
405 410 415

Trp Lys

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1148 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Maize
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..1148
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GA GAG CAC ATC CAT GAC CTG CAG CTC CAG ATC CGG CAG AAG ACC CAT 47
Glu His Ile His Asp Leu Gln Leu Gln Ile Arg Gln Lys Thr His
1 5 10 15

AAC CTC AAC CGC CTC GAG GCC CAG CGC AAC GAC CTC AAC TCC CGA GTT 95
Asn Leu Asn Arg Leu Ala Gln Arg Asn Asp Leu Asn Ser Arg Val
20 25 30

AGA ATG CTC AGG GAA GAG TTG CAG TTG CTT CAA GAG CCT GGC TCA TAT 143
Arg Met Leu Arg Glu Leu Gln Leu Gln Glu Pro Gly Ser Tyr
35 40 45

GTT GGT GAG GTG GTG AAG GTC ATG GGG AAA TCA AAG GTT CTG GTG AAG 191
Val Gly Val Val Lys Val Met Gly Lys Ser Lys Val Leu Val Lys
50 55 60

GTA CAT CCC GAA GGC AAA TAT GTG GTG GAT ATA GAT AAG AGC ATT GAT 239
Val His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys Ser Ile Asp
65 70 75

ATC ACT AAG ATC ACA CCT TCA ACA AGA GTT GCT CTT CGG AAT GAC AGC 287
Ile Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg Asn Asp Ser
80 85 90 95

TAT ATG CTC CAT CTG ATC CTA CCA AGC AAA GTT GAT CCA TTG GTC AAT 335
Tyr Met Leu His Leu Ile Leu Pro Ser Lys Val Asp Pro Leu Val Asn
100 105 110

CTC ATG AAA GTT GAG AAG GTT CCG GAT TCT ACC TAT GAT ATG ATT GGA Leu Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp Met Ile Gly 115 120 125	383
GGC CTT GAC CAG CAA ATT AAA GAG ATC AAA GAG GTC ATT GAG CTT CCA Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile Glu Leu Pro 130 135 140	431
ATC AAA CAT CCG GAA CTG TTT GAG AGC CTT GGA ATT GCG CAA CCA AAG Ile Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala Gln Pro Lys 145 150 155	479
GGT GTC CTT CTT TAT GGA CCT CCG GGC ACA GGA AAG ACA TTG TTG GCA Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala 160 165 170 175	527
CGT GCG GTT GCT CAT CAC ACT GAC TGC ACC TTC ATC AGG GTG TCT GGT Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg Val Ser Gly 180 185 190	575
TCT GAG TTG GTT CAG AAG TAT ATT GGT GAG GGC TCC CGG ATG GTT AGG Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg Met Val Arg 195 200 205	623
GAA CTC TTT GTT ATG GCC AGG GAA CAT GCA CCA TCC ATT ATA TTT ATG Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile Ile Phe Met 210 215 220	671
GAT GAA ATT GAC TCT ATC GGA TCT GCT AGA ATG GAG TCT GGA ACT GGC Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser Gly Thr Gly 225 230 235	719
AAC GGT GAC AGT GAA GTT CAG CGT ACT ATG CTT GAA CTT CTA AAC CAG Asn Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu Leu Asn Gln 240 245 250 255	767
CTC GAT GGT TTT GAA GCA TCA AAC AAA ATT AAG GTT TTG ATG GCA ACG Leu Asp Gly Phe Ala Ser Asn Lys Ile Lys Val Leu Met Ala Thr 260 265 270	815
AAC AGA ATA GAC ATT TTG GAT CAA GCC CTT CTG AGG CCT GGC CGC ATA Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro Gly Arg Ile 275 280 285	863
GAC AGG AAG ATT GAA TTT CCA AAT CCT AAC GAG GAT TCA CGT TTC GAT Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Asp Ser Arg Phe Asp 290 295 300	911
ATC TTG AAG ATC CAT TCA AGA AAA ATG AAC TTG ATG CGT GGC ATT GAT Ile Leu Lys Ile His Ser Arg Lys Met Asn Leu Met Arg Gly Ile Asp 305 310 315	959
CTG AAA AAG ATC GCG GAA AAG ATG AAT GGG GCC TCA GGA GCT GAG CTC Leu Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser Gly Ala Glu Leu 320 325 330 335	1007
AAG GCC GTC TGC ACA GAG GCT GGA ATG TTT GCT CTT CGT GAG AGA AGG Lys Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg Glu Arg Arg 340 345 350	1055
GTC CAC GTT ACC CAG GAG GAC TTC GAG ATG GCA GTG GCC AAG GTG ATG Val His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala Lys Val Met 355 360 365	1103

AAG AAA GAC ACG GAG AAG AAC ATG TCC CTG CGC AAG CTC TGG AAG
 Lys Lys Asp Thr Glu Lys Asn Met Ser Leu Arg Lys Leu Trp Lys
 370 375 380

1148

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu His Ile His Asp Leu Gln Leu Gln Ile Arg Gln Lys Thr His Asn
 1 5 10 15

Leu Asn Arg Leu Glu Ala Gln Arg Asn Asp Leu Asn Ser Arg Val Arg
 20 25 30

Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro Gly Ser Tyr Val
 35 40 45

Gly Glu Val Val Lys Val Met Gly Lys Ser Lys Val Leu Val Lys Val
 50 55 60

His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys Ser Ile Asp Ile
 65 70 75 80

Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg Asn Asp Ser Tyr
 85 90 95

Met Leu His Leu Ile Leu Pro Ser Lys Val Asp Pro Leu Val Asn Leu
 100 105 110

Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp Met Ile Gly Gly
 115 120 125

Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile Glu Leu Pro Ile
 130 135 140

Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala Gln Pro Lys Gly
 145 150 155 160

Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Arg
 165 170 175

Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg Val Ser Gly Ser
 180 185 190

Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg Met Val Arg Glu
 195 200 205

Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile Ile Phe Met Asp
 210 215 220

Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser Gly Thr Gly Asn
 225 230 235 240

Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu Leu Asn Gln Leu
 245 250 255

Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val Leu Met Ala Thr Asn
 260 265 270

Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro Gly Arg Ile Asp
 275 280 285
 Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Asp Ser Arg Phe Asp Ile
 290 295 300
 Leu Lys Ile His Ser Arg Lys Met Asn Leu Met Arg Gly Ile Asp Leu
 305 310 315 320
 Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser Gly Ala Glu Leu Lys
 325 330 335
 Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg Glu Arg Arg Val
 340 345 350
 His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala Lys Val Met Lys
 355 360 365
 Lys Asp Thr Glu Lys Asn Met Ser Leu Arg Lys Leu Trp Lys
 370 375 380

2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCAAGCCAA	CAAGCAAGAC	CGCTTCTGCT	TGTGATCCGA	AACCTTCCTT	CGAACGCAAA	60
AAGAACCCCCA	CCCGACGTAC	CGCGAGCCGG	CGATGGCGAC	GGTGGCGATG	GACATCTCGA	120
AGCCCACGCC	GGCAGCGTCC	GGTGACGAGG	CAGCAGCGGC	GGCGAAGGGG	AGGAGCAGCG	180
GCGGGGCGA	GGGGCTGCGG	CAGTACTACC	TGCAGCACAT	CCATGACCTG	CAGCTCCAGA	240
TCCGGCAGAA	GACCCATAAC	CTCAACCGCC	TCGAGGCCA	GCGCAACGAC	CTCAACTCCC	300
GAGTTAGAAT	GCTCAGGGAA	GAGTTGCAGT	TGCTTCAAGA	GCCTGGCTCA	TATGTTGGTG	360
AGGTGGTGA	GGTCATGGGG	AAATCAAAGG	TTCTGGTGAA	GGTACATCCC	GAAGGCAAAT	420
ATGTGGTGA	TATAGATAAG	AGCATTGATA	TCACTAAGAT	CACACCTTCA	ACAAGAGTTG	480
CTCTTCGGAA	TGACAGCTAT	ATGCTCCATC	TGATCCTACC	AAGCAAAGTT	GATCCATTGG	540
TCAATCTCAT	GAAAGTTGAG	AAGGTTCCGG	ATTCTACCTA	TGATATGATT	GGAGGCCTTG	600
ACCAGCAAAT	TAAAGAGATC	AAAGAGGTCA	TTGAGCTTCC	AATCAAACAT	CCGGAACGT	660
TTGAGAGCCT	TGGAATTGCG	CAACCAAAGG	GTGTCCTTCT	TTATGGACCT	CCGGGCACAG	720
GAAAGACATT	GTTGGCACGT	GC GGTTGCTC	ATCACACTGA	CTGCACCTTC	ATCAGGGTGT	780
CTGGTTCTGA	GTTGGTTCA	AGTATATTG	GTGAGGGCTC	CCGGATGGTT	AGGAACTCT	840
TTGTTATGGC	CAGGGAACAT	GCACCATCCA	TTATATTTAT	GGATGAAATT	GACTCTATCG	900
GATCTGCTAG	AATGGAGTCT	GGAACTGGCA	ACGGTGACAG	TGAAGTTCA	CGTACTATGC	960
TTGAACCTCT	AAACCAAGCTC	GATGGTTTG	AAGCATCAA	CAAATTAAG	GTGTTGATGG	1020

CAACGAACAG AATAGACATT TTGGATCAAG CCCTTCTGAG GCCTGGCCGC ATAGACAGGA	1080
AGATTGAATT TCCAATCCT AACGAGGATT CACGTTTCGA TATCTTGAAG ATCCATTCAA	1140
GAAAAATGAA CTTGATGCGT GGCATTGATC TGAAAAAGAT CGCGGAAAAG ATGAATGGGG	1200
CCTCAGGAGC TGAGCTCAAG GCCGTCTGCA CAGAGGCTGG AATGTTGCT CTTCGTGAGA	1260
GAAGGGTGCA CGTTACCCAG GAGGACTTCG AGATGGCAGT GGCCAAGGTG ATGAAGAAAG	1320
ACACGGAGAA GAACATGTCC CTGCGCAAGC TCTGGAAG	1358

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 422 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Thr Val Ala Met Asp Ile Ser Lys Pro Thr Pro Ala Ala Ser
 1 5 10 15

Gly Asp Glu Ala Ala Ala Ala Lys Gly Arg Ser Gly Gly Gly
 20 25 30

Glu Gly Leu Arg Gln Tyr Tyr Leu Gln His Ile His Asp Leu Gln Leu
 35 40 45

Gln Ile Arg Gln Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg
 50 55 60

Asn Asp Leu Asn Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu
 65 70 75 80

Leu Gln Glu Pro Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly
 85 90 95

Lys Ser Lys Val Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val
 100 105 110

Asp Ile Asp Lys Ser Ile Asp Ile Thr Lys Ile Thr Pro Ser Thr Arg
 115 120 125

Val Ala Leu Arg Asn Asp Ser Tyr Met Leu His Leu Ile Leu Pro Ser
 130 135 140

Lys Val Asp Pro Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp
 145 150 155 160

Ser Thr Tyr Asp Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile
 165 170 175

Lys Glu Val Ile Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser
 180 185 190

Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly
 195 200 205

Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys
 210 215 220

Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly
 225 230 235 240
 Glu Gly Ser Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His
 245 250 255
 Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala
 260 265 270
 Arg Met Glu Ser Gly Thr Gly Asn Gly Asp Ser Glu Val Gln Arg Thr
 275 280 285
 Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys
 290 295 300
 Ile Lys Val Leu Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala
 305 310 315 320
 Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro
 325 330 335
 Asn Glu Asp Ser Arg Phe Asp Ile Leu Lys Ile His Ser Arg Lys Met
 340 345 350
 Asn Leu Met Arg Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn
 355 360 365
 Gly Ala Ser Gly Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met
 370 375 380
 Phe Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu
 385 390 395 400
 Met Ala Val Ala Lys Val Met Lys Lys Asp Thr Glu Lys Asn Met Ser
 405 410 415
 Leu Arg Lys Leu Trp Lys
 420

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mouse
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Leu Asp Gly Pro Glu Gln Met Glu Leu Glu Glu Gly Lys Ala
 1 5 10 15

Gly Ser Gly Leu Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln
 20 25 30

Leu Ile Val Asn Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln
 35 40 45

Arg Asn Glu Leu Asn Ala Lys Val Arg Leu Leu Arg Glu Glu Leu Gln
 50 55 60

Leu Leu Gln Glu Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met
 65 70 75 80
 Asp Lys Lys Lys Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val
 85 90 95
 Val Asp Val Asp Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys
 100 105 110
 Arg Val Ala Leu Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro
 115 120 125
 Asn Lys Val Asp Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro
 130 135 140
 Asp Ser Thr Tyr Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu
 145 150 155 160
 Ile Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu
 165 170 175
 Ala Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro
 180 185 190
 Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp
 195 200 205
 Cys Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile
 210 215 220
 Gly Glu Gly Ala Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu
 225 230 235 240
 His Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser
 245 250 255
 Ser Arg Leu Glu Gly Gly Ser Gly Gly Asp Ser Glu Val Gln Arg Thr
 260 265 270
 Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn
 275 280 285
 Ile Lys Val Ile Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Ser Ala
 290 295 300
 Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro
 305 310 315 320
 Asn Glu Glu Ala Arg Leu Asp Ile Leu Lys Ile His Ser Arg Lys Met
 325 330 335
 Asn Leu Thr Arg Gly Ile Asn Leu Arg Lys Ile Ala Glu Leu Met Pro
 340 345 350
 Gly Ala Ser Gly Ala Glu Val Lys Gly Val Cys Thr Glu Ala Gly Met
 355 360 365
 Tyr Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu
 370 375 380
 Met Ala Val Ala Lys Val Met Gln Lys Asp Ser Glu Lys Asn Met Ser
 385 390 395 400
 Ile Lys Lys Leu Trp Lys
 405

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Thr	Ala	Ala	Val	Thr	Ser	Ser	Asn	Ile	Val	Leu	Glu	Thr	His	Glu
1						5				10				15	
Ser	Gly	Ile	Lys	Pro	Tyr	Phe	Glu	Gln	Lys	Ile	Gln	Glu	Thr	Glu	Leu
		20					25				30				
Lys	Ile	Arg	Ser	Lys	Thr	Glu	Asn	Val	Arg	Arg	Leu	Glu	Ala	Gln	Arg
		35				40				45					
Asn	Ala	Leu	Asn	Asp	Lys	Val	Arg	Phe	Ile	Lys	Asp	Glu	Leu	Arg	Leu
		50				55				60					
Leu	Gln	Glu	Pro	Gly	Ser	Tyr	Val	Gly	Glu	Val	Ile	Lys	Ile	Val	Ser
		65				70			75			80			
Asp	Lys	Lys	Val	Leu	Val	Lys	Val	Gln	Pro	Glu	Gly	Lys	Tyr	Ile	Val
		85				90				95					
Asp	Val	Ala	Lys	Asp	Ile	Asn	Val	Lys	Asp	Leu	Lys	Ala	Ser	Gln	Arg
		100				105				110					
Val	Cys	Leu	Arg	Ser	Asp	Ser	Tyr	Met	Leu	His	Lys	Val	Leu	Glu	Asn
		115				120				125					
Lys	Ala	Asp	Pro	Leu	Val	Ser	Leu	Met	Met	Val	Glu	Lys	Val	Pro	Asp
		130				135				140					
Ser	Thr	Tyr	Asp	Met	Val	Gly	Gly	Leu	Thr	Lys	Gln	Ile	Lys	Glu	Ile
		145				150				155			160		
Lys	Glu	Val	Ile	Glu	Leu	Pro	Val	Lys	His	Pro	Glu	Leu	Phe	Glu	Ser
		165				170				175					
Leu	Gly	Ile	Ala	Gln	Pro	Lys	Gly	Val	Ile	Leu	Tyr	Gly	Pro	Pro	Gly
		180				185				190					
Thr	Gly	Lys	Thr	Leu	Leu	Ala	Arg	Ala	Val	Ala	His	His	Thr	Asp	Cys
		195				200				205					
Lys	Phe	Ile	Arg	Val	Ser	Gly	Ala	Glu	Leu	Val	Gln	Lys	Tyr	Ile	Gly
		210				215				220					
Glu	Gly	Ser	Arg	Met	Val	Arg	Glu	Leu	Phe	Val	Met	Ala	Arg	Glu	His
		225				230				235			240		
Ala	Pro	Ser	Ile	Ile	Phe	Met	Asp	Glu	Ile	Asp	Ser	Ile	Gly	Ser	Thr
		245				250				255					
Arg	Val	Glu	Gly	Ser	Gly	Gly	Asp	Ser	Glu	Val	Gln	Arg	Thr	Met	
		260				265				270					

Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Thr Ser Lys Asn Ile
 275 280 285
 Lys Ile Ile Met Ala Thr Asn Arg Leu Asp Ile Leu Asp Pro Ala Leu
 290 295 300
 Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro Ser
 305 310 315 320
 Val Ala Ala Arg Ala Glu Ile Leu Arg Ile His Ser Arg Lys Met Asn
 325 330 335
 Leu Thr Arg Gly Ile Asn Leu Arg Lys Val Ala Glu Lys Met Asn Gly
 340 345 350
 Cys Ser Gly Ala Asp Val Lys Gly Val Cys Thr Glu Ala Gly Met Tyr
 355 360 365
 Ala Leu Arg Glu Arg Arg Ile His Val Thr Gln Glu Asp Phe Glu Leu
 370 375 380
 Ala Val Gly Lys Val Met Asn Lys Asn Gln Glu Thr Ala Ile Ser Val
 385 390 395 400
 Ala Lys Leu Phe Lys
 405

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human Trip1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Leu Asp Gly Pro Glu Gln Met Glu Leu Glu Glu Gly Lys Ala
 1 5 10 15
 Gly Ser Gly Leu Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln
 20 25 30
 Leu Ile Val Asn Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln
 35 40 45
 Arg Asn Glu Leu Asn Ala Lys Val Arg Leu Leu Arg Glu Glu Leu Gln
 50 55 60
 Leu Leu Gln Glu Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met
 65 70 75 80
 Asp Lys Lys Lys Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val
 85 90 95
 Val Asp Val Asp Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys
 100 105 110
 Arg Val Ala Leu Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro
 115 120 125

Asn Lys Val Asp Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro
 130 135 140
 Asp Ser Thr Tyr Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu
 145 150 155 160
 Ile Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu
 165 170 175
 Ala Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro
 180 185 190
 Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp
 195 200 205
 Cys Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile
 210 215 220
 Gly Glu Gly Ala Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu
 225 230 235 240
 His Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser
 245 250 255
 Ser Arg Leu Glu Gly Gly Ser Gly Ser Ser Glu Val Gln Arg Gln
 260 265 270
 Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn
 275 280 285
 Ile Lys Val Ile Met Ala Thr Asn Arg Ile Asp Met Leu Asp Ser Ala
 290 295 300
 Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro
 305 310 315 320
 Asn Glu Glu Ala Arg Leu Asp Ile Leu Lys Ile His Ser Arg Lys Met
 325 330 335
 Asn Leu Thr Arg Gly Ile Asn Leu Arg Lys Ile Ala Glu Leu Met Pro
 340 345 350
 Gly Ala Ser Gly Ala Glu Val Lys Gly Val Cys Thr Glu Ala Gly Met
 355 360 365
 Tyr Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu
 370 375 380
 Met Ala Val Ala Lys Val Met Gln Lys Asp Ser Glu Lys Asn Met Ser
 385 390 395 400
 Ile Lys Lys Leu Trp Lys
 405

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human p45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Leu Asp Gly Pro Glu Gln Met Glu Leu Glu Glu Gly Lys Ala
 1 5 10 15

Gly Ser Gly Leu Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln
 20 25 30

Leu Ile Val Asn Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln
 35 40 45

Arg Asn Glu Leu Asn Ala Lys Val Arg Leu Leu Arg Arg Glu Leu Gln
 50 55 60

Leu Leu Gln Glu Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met
 65 70 75 80

Asp Lys Lys Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val
 85 90 95

Val Asp Val Asp Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys
 100 105 110

Arg Val Ala Leu Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro
 115 120 125

Asn Lys Val Asp Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro
 130 135 140

Asp Ser Thr Tyr Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu
 145 150 155 160

Ile Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu
 165 170 175

Ala Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro
 180 185 190

Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp
 195 200 205

Cys Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile
 210 215 220

Gly Glu Gly Ala Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu
 225 230 235 240

His Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser
 245 250 255

Ser Arg Leu Glu Gly Gly Ser Gly Gly Asp Ser Glu Val Gln Arg Thr
 260 265 270

Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn
 275 280 285

Ile Lys Val Ile Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Ser Ala
 290 295 300

Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro
 305 310 315 320

Asn Glu Glu Ala Arg Leu Asp Ile Leu Lys Ile His Ser Arg Lys Met
 325 330 335

Asn Leu Thr Arg Gly Ile Asn Leu Arg Lys Ile Ala Glu Leu Met Pro
 340 345 350

Gly Ala Ser Gly Ala Glu Val Lys Gly Val Cys Thr Glu Ala Gly Met
 355 360 365

Tyr Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu
 370 375 380

Met Ala Val Ala Lys Val Met Gln Lys Asp Ser Glu Lys Asn Met Ser
 385 390 395 400

Ile Lys Lys Leu Trp Lys
 405

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: w11n.pk0053.g3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCCGACCGA CCTACCCCTAA TCGGGCATGG CGACGGTGGC GATGGACATC TCGAAGCCCA	60
CTCCAGTGGC GTCCGGCGAC GAGGCCGCGG CGGCGGCCAA GGGGAGGAGC GGCGGAGGGG	120
GCGAGGGGCT GCGGCAGTAC TACCTGCAGC ACATCCACGA CCTGCAGCTC CAGATCCGGC	180
ATAAGACCCA CAACCTAAC CGTCTCGAGG CCCAGCGCAA TGACCTAAC TCCCGAGTTA	240
GAATGCTCAG GGAAGATTGC ANTTGCTTCA NGAGCCTGGC TCATATGTTG GTNAGGTGGT	300
GAAGGCATGG GGAAATCAAA GGTTCTGGGT NAAGGTAAAC CCCGAAGGCA AATANNTTGT	360
TGATATAAT AANCCATTGA TTCNCANGTT NACACCTNCA ACAANANCAC CTTCGAANTG	420
ATACNANNNGC CCATCTGTTT TACCACCAAA TTNNCATTGG CAACCCCATG AANTAAAAG	480
TCCTGATCAC ATAAAANCTT TGGGGCCTGC CACCCATTAG AAATANNGTT CTTGTTCAA	540
NAAAAACGG	548

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: w11n.pk0053.g3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Thr Val Ala Met Asp Ile Ser Lys Pro Thr Pro Val Ala Ser
 1 5 10 15

Gly Asp Glu Ala Ala Ala Ala Lys Gly Arg Ser Gly Gly Gly Gly
 20 25 30

Glu Gly Leu Arg Gln Tyr Tyr Leu Gln His Ile His Asp Leu Gln Leu
 35 40 45

Gln Ile Arg His Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg
 50 55 60

Asn Asp Leu Asn Ser Arg Val Arg Met Leu Arg Glu Asp Xaa Xaa Leu
 65 70 75 80

Leu Xaa Glu Pro Gly Ser Tyr Val Gly Xaa Val Val Lys Ala Trp Gly
 85 90 95

Asn Gln Arg Phe Trp Val Lys Val Asn Pro Glu Gly Lys Xaa Xaa Val
 100 105 110

Asp Ile Asn
 115

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 593 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: rlr6.pk0064.e10
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTTTAAACGG TACAGGAAAA ACGCTACTAG CTCGGGCAGT TGCTCATCAC ACCGACTGTA	60
CCTTATTAA GGGTGTCAAG TTCCGAGTTG GTTCAGAAGT ATATTGGAGA GGGTTCCAGA	120
ATGGTTCGTG AACTATTGT GATGCCANA GAGCATGCAC CATCCATAAT CTTTATGGAT	180
GAAATAGACT CCATTGGATC TGCTANAATG CAGTCANGAT CTGGGGTGG TGATAGTGAG	240
GTTCAACGCA CTATGCTTGA TCTTCTGAAT CAACTTGATG GCTTTGAAGC ATCAAACANA	300
ATTAAGGTCT TATGGCGACA AATANGATGG ATATTTGGA TCAAGCTCTC TGANGCCTGG	360
TCGCATTGAT AGGAAGATGA ATTTCCAATC CGAATGAAGA TCCGCTTGAT ANTTGAAGAT	420
CATTCAAGAA AAATGACTGA TCTGGATTGT CTGAAAAGAT GCAGAGAAAT GATGGGCNCT	480
GGACAAACTA AGNGTCTNAC GAACAAGATT TGCCTCCAAA NAGGTATTCA CAGAGATCTA	540
TGGGTGCAAG GTGAAAGNAC GAAGAATCCG NCACCGAATA AGANNACCCA ACC	593

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: rlr6.pk0064.e10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp
1 5 10 15

Cys Thr Phe Xaa Arg Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile
20 25 30

Gly Glu Gly Ser Arg Met Val Arg Glu Leu Phe Val Met Ala Xaa Glu
35 40 45

His Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser
50 55 60

Ala Xaa Met Gln Ser Xaa Ser Gly Gly Asp Ser Glu Val Gln Arg
65 70 75 80

Thr Met Leu Asp Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn
85 90 95

Xaa Ile Lys Val Xaa Met Ala Thr Asn Xaa Met Asp Ile Leu Asp Gln
100 105 110

Ala Leu Xaa Xaa Pro Gly Arg Ile Asp Arg Lys Met Asn Phe
115 120 125